

OM protein - protein search, using sw model
 Run on: MY 18, 2002, 02:18:14 ; Search time 67.56 Seconds
 Scoring table: BLOSUM62
 Searched: 283138 seqs, 96089334 residues
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

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GenCore version 4.5

SUMMARIES

Copyright (c) 1993 - 2000 Gencore version OM protein - protein search, using sw model
Run on: May 18, 2002, 02:18:14 ; Searcher:
Title: US-09-719-748-2
Perfect score: 1846
Sequence: 1 MEPFKQOKVDFYDIEEGL...
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 283138 seqs. 96089334 residues

RESULT 2

T32930 hypothetical protein K12C11.4 - Caeenorhabditis elegans

C;Species: Caeenorhabditis elegans

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 31-Jan-2000

C;Accession: T32930

R;Wansley, P.; Kramer, J.

A;Description: The sequence of C. elegans cosmid K12C11.

A;Reference number: Z21248

A;Accession: T32930

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-1435 <WAM>

A;Cross-references: EMBL:AF043701; PIDN:AAB97579.1; GSDB:GN0019; CESP:K12C11.4

A;Experimental source: strain Bristol N2; clone K12C11

C;Genetics:

A;Gene: CESP:K12C11.4

A;Map position: 1

A;Introns: 79/2; 154/2; 267/2; 433/1; 533/3; 599/3; 691/3; 875/1; 1025/3; 1169/3; 1348/3

C;Superfamily: death-associated protein kinase; ankyrin repeat homology; protein kinase

Query Match 42.6%; Score 787; DB 2; Length 1435;

Best Local Similarity 42.5%; Pred. No. 1. 1e-25;

Matches 160; Conservative 63; Mismatches 105; Indels 6; Gaps 4;

Qy 22 GCFATVKKCREKSTGLEYAAFKIKRROSARSGRSREETERESVSIROYL-HHNVITLH 80

Db 80 GQFAVVRRVRDRKTGEYAAFKIKRKYATSSRGVVRONIEREVRLQKIRGNNSNVELH 139

Qy 81 DYENNTDWHILELYSGEFLFLAQKESSEEATFIKOILGVNYIHTKIAHFDL 140

Db 140 AVYETASDVITLVEELVGGELFDHVCAKECLDEVEAAFKIQILLAVRHLSLHTVHLI 199

Qy 141 KFENIMLDKIPKIPHIKLIDGLAHEIEDVGFKNIFPEPVAEIVNYPEGLEADM 200

Db 200 KPFENVNL-KGPGSOKI-KGPGSOKI-LDFGLSRBIEPGAVVKOMVGPPEPVAEIVNYPEGLEADM 257

Qy 201 WSIGVTVILLSGASPLFLGDTKQETLANTISVSYDFDEEFSTSLAKDFIRKLKVET 260

Db 258 WAVGVTVILLSGGSPFLGDNDRDETSNITRVYHSDRVKNTSKHAKDFIYLRVVD 317

Qy 261 RKRLTIOALRIPWIPVPUQAMVREVRSEVNLENRERKQYRRWILSFSTVSLCNHLTR 320

Db 318 DORATVECLOHPWIPEGNAIDKASCITISHQSFKTRQRWKRCVCELMVLLKASK 377

Qy 321 SIMKKVHLRPDED-LRNCESTEETARRAHL 352

Db 378 SRRISGGRFDEDMVASCILCAEE-GNLRALH 410

RESULT 4

A59307 myosin-light-chain kinase (EC 2.7.1.117), smooth muscle - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Accession: A59307; A41674; B41674; A40210

R;Gallagher, P.J.; Herring, B.P.; Griffin, S.A.; Stull, J.T.

J; Biol. Chem. 266, 23936-23944, 1991

A;Title: Molecular characterization of a mammalian smooth muscle myosin light chain kinase

A;Reference number: A41674; MUID:92084694

A;Accession: A59307

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-147 <GA>

A;Cross-references: GB:M76233; PIDN:9165703; PIDN:AA73093.1; PID:9165704

A;Experimental source: dev stage Adult; sex Female; tissue type smooth muscle

A;Note: this revision submission is not cited in GenBank entry RABSMMLCKR, release 11

A;Accession: A41674

A;Molecule type: mRNA

A;Residues: 1-738 <RO>; 741-1147 <GA>

A;Cross-references: GI:M76233

A;Note: the sequence is revised in GenBank entry RABSMMLCKR, release 115, (PIDN:AA73093.1; MUID:92084694)

A;Accession: B41674

RESULT 3

JN0583 myosin-light-chain kinase (EC 2.7.1.117) 155k protein - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 20-Apr-2000

A;Molecule type: DNA
A;Residues: 1-22, CTA, 26, 'SRS' <GA2>
A;Cross-references: GB:M76369
A;Note: this translation is not annotated in GenBank entry RABSMMLKD, release 115
A;Title: R.Gallagher, P.J.; Herring, B.P.; Griffin, S.A.; Stull, J.T.
J. Biol. Chem. 267, 9450, 1992
A;Reference number: A40210; MUID:92250555
A;Contents: erratum
A;Accession: A40210
A;Molecule type: DNA
A;Residues: 23-30 <GA3>
A;Note: this is a revision to the sequence B41674 from reference A41674
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; fibronectin type III
C;Keywords: ATP; phosphotransferase; smooth muscle
P;443-403/Domain: immunoglobulin homology <IMM1>
F;694-931/Domain: protein kinase homology <KIN>
F;702-710/Region: protein kinase ATP-binding motif
F;1055-1116/Domain: immunoglobulin homology <IMM2>

Query Match 37.6%; Score 694; DB 2; Length 117;
Best Local Similarity 41.6%; Pred. No. 6.2e-22;
Matches 146; Conservative 53; Mismatches 120; Indels 22; Gaps 6;
Oy 6 QKVKEDFYDIDGEGSGQFAIVKVKCREKSTGLEYAAKTKRROSRSRGSVREIEREV 65
Db 689 EOKVSDPFIDIEERLGGSKFGQVFLVEKTKWAGKFKKAYSRAK-----EKENIPAEI 742
Oy 66 SILRQLVLRHNVITLHDVYENRTDVHILEVSGLAEELDAQKESLSEEATSFIKIL 124
Db 743 GIMNCNLHHPKLVQCVDAFEERKANTVMLVLEIVSGLSEELFERTIDDEFELTERECIKYMRQS 802
Qy 125 DGVNVLHTRKKIAHDLKPEIMILDKNIPIPHIKLIDGLAHELEDGEFEKNIFGTPEEV 184
Db 803 EGVEYIHKGOTVHILDKENIMCNYKT--GTRIKLIDGLARRLLENAGSLKVIEGTPEV 860
Qy 185 APETVNVEPLGLEADMWSGVTVYILSGASPLFGDTKQETLANTITSVSYDFDEEFHT 244
Db 861 APEVINYEPISIATDMWSIGVIVCYILVSGLSPFMGDNDNETLAVTSATWDFFDEAFEI 920
Qy 245 SELAKDFERKLVLUKTRERLTQBALRPWI--PVUDNOQAMMVERSVNLERKQVYR 303
Db 921 SDDAKDFISNLKLKDKMKRDLCTQLOHWWLMKOTKNEA---KKLSKDRKYMARR 975
Oy 304 RWHLFSVSLCNHLTRSLM-----KKVHLRDPEDURNCESDEEDiar 347
Db 976 KMQTKGNVAVRAGRLSSHAMISLGSRSSTSPTSPPTAERIETEEDYSQ 1026

RESULT 5

S68235 myosin-light-chain kinase (EC 2.7.1.117), 210K, nonmuscle - chicken
C;Species: Gallus gallus (chicken)
C;Accession: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Date: 10-Sep-1999
C;Accession: S68235; MUID:96033976
R;Waterson, D.M.; Collings, M.; Lukas, T.J.; Van Edik, L.J.; Birukov, K.G.; Stepanova, FERS Lett. 373, 217-220, 1995
A;Title: Multiple gene products are produced from a novel protein kinase transcription
A;Reference number: S68235; MUID:96033976
A;Accession: S68235
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1906 <WAT>
A;Cross-references: EMBL:X52876; NID:992992; PIDN:CAA37056.1; PID:992993
R;Shoemaker, M.O.; Lau, W.; Shattuck, R.L.; Kwiatkowski, A.P.; Matrisian, P.E.; Guerra-S
J. Cell Biol. 111, 1107-1125, 1990
A;Title: Use of DNA sequence and mutant analyses and antisense oligodeoxynucleotides to
A;Reference number: A37099; MUID:90361738
A;Accession: A37099
A;Molecule type: mRNA

A;Residues: 649-1906 <SHO>
A;Cross-references: EMBL:X52876
R;Collinge, M.; Matrisian, P.E.; Zimmer, W.E.; Shattuck, R.L.; Lukas, T.J.; Van Eldi
Mol. Cell. Biol. 12, 2359-2371, 1992
A;Title: Structure and expression of a calcium-binding protein gene contained within
A;Reference number: A44389; MUID:92236611
A;Accession: B44389
A;Status: preliminary
A;Molecule type: DNA
A;Cross-references: GB:MB8284; NID:9212237; PIDN:AAB53767.1; PID:9212238
A;Accession: M4389
A;Status: preliminary
A;Molecule type: mRNA
A;Accession: 1655-1906 <COL>
A;Cross-references: GB:MB8284
A;Status: preliminary
A;Molecule type: DNA
A;Accession: S28227
A;Cross-references: EMBL:M96655; NID:9212744; PIDN:AAA49083.1; PID:9212745
A;Cross-references: S78216
A;Molecule type: DNA
A;Residues: 1750-1906 <ON>
A;Cross-references: EMBL:M96987
R;Olson, N.J.; Pearson, R.B.; Needelman, D.S.; Hurwitz, M.Y.; Kemp, B.E.; Means, A.R.
PROC. Natl. Acad. Sci. U.S.A. 87, 2284-2288, 1990
R;Yoshikai, S.I.; Ikebe, M. Arch. Biochem. Biophys. 299, 242-247, 1992
A;Title: Molecular cloning of the chicken gizzard telokin gene and cDNA.
A;Reference number: S28227; MUID:93073972
A;Accession: 1750-1906 <YOS>
A;Molecule type: mRNA
A;Cross-references: EMBL:M96655; NID:9212744; PIDN:AAA49083.1; PID:9212745
A;Cross-references: S78216
A;Molecule type: DNA
A;Residues: 1750-1906 <ON>
A;Cross-references: EMBL:M96987
R;Guerrero Jr., V.; Russo, M.A.; Olson, N.J.; Putkey, J.A.; Means, A.R.
Biochemistry 25, 872-881, 1986
A;Title: Domain organization of chicken gizzard myosin light chain deduced fr
A;Reference number: A25810; MUID:8715787
A;Accession: A25810
A;Molecule type: mRNA
A;Cross-references: GB:W31048; NID:9212660; PIDN:AAA49069.1; PID:9212661
R;Guerrero Jr., V.; Russo, M.A.; Olson, N.J.; Putkey, J.A.; Means, A.R.
Biochemistry 25, 872-881, 1986
A;Title: Domain organization of chicken gizzard myosin light chain deduced fr
A;Reference number: A25810; MUID:8715787
A;Accession: A25810
A;Molecule type: mRNA
A;Residues: 1258-1438, 'Q', 1440-1905 <GUE>
C;Genetics:
A;Introns: 1735/3; 1779/1; 1819/1
C;Superfamily: myosin-light-chain kinase, nonmuscle; fibronectin type III repeat hom
C;Keywords: alternative initiators; ATP; calmodulin binding; phosphoprotein; phospho
F;512-599/Domain: immunoglobulin homology <IMM1>
F;935-1906/Product: myosin-light-chain kinase, 108K, smooth muscle (from 5.5kb trans
F;1098-1158/Domain: protein kinase homology <IMM2>
F;1451-1708/Domain: protein kinase homology <KIN>
F;1459-1667/Region: protein kinase ATP-binding motif
F;1808-1869/Domain: immunoglobulin homology <IMM3>
Query Match 37.1%; Score 685.5; DB 1; Length 1906;
Best Local Similarity 43.8%; Pred. No. 2.2e-21;
Matches 140; Conservative 58; Mismatches 107; Indels 15; Gaps 5;
Oy 6 QKVKEDFYDIDGEGSGQFAIVKVKCREKSTGLEYAAKTKRROSRSRGSVREIEREV 65
Db 1446 EOKVSDPFIDIEERLGGSKFGQVFLVEKTKWAGKFKKAYSRAK-----EKENIPAEI 1499
Oy 66 SILRQLVLRHNVITLHDVYENRTDVHILEVSGLAEELDAQKESLSEEATSFIKIL 124
Db 1500 SIMNCNLHHPKLVQCVDAFEERKANTVMLVLEVSGLSEELFERTIDDEFELTERECIKYMRQS 1559
Oy 125 DGVNVLHTRKKIAHDLKPEIMILDKNIPIPHIKLIDGLAHELEDGEFEKNIFGTPEEV 184
Db 1560 EGVEYIHKGOTVHILDKENIMCNYKT--GTSIKLIDGLARRLESASLKVIEGTPEEV 1617

QY 185 APEIVNYEPLGLEADMNSIGVITYIILSGASPLFLGDTKQETLANTISVSYDFDEFSHT 244
 |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 1618 APEIVNYEPLGLEADMNSIGVITYIILSGASPLFLGDTKQETLANTISVSYDFDEFSHT 244
 |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 C;Species: Rattus norvegicus (Norway rat)
 C;Accession: JG7733; RC7178
 R;Matsumoto, M.; Miyake, Y.; Nagita, M.; Inoue, H.; Shirakubo, D.; Takemoto, K.; Ohtsuka
 J.; Matsumoto, M.; Miyake, Y.; Nagita, M.; Inoue, H.; Shirakubo, D.; Takemoto, K.; Ohtsuka
 A;Title: A serine/threonine kinase which causes apoptosis-like cell death interacts with
 A;Content: Brain
 A;Accession: JG7733
 A;Molecule type: mRNA

QY 245 SELAKDFIRKLKVTRKRTIQEALRHPWIT 303
 |||:|||:|||:|||:|||:|||:|||:
 Db 1678 SDDAKDFISNLKQMKSRLNCTQCLQHPLQKTDKTMKA-----KKLSKDRMKYMAR 1732
 |||:|||:|||:|||:|||:|||:
 C;Species: Caenorhabditis elegans
 C;Accession: T3416
 R;Fulton, B.; Wohlgemann, P.
 Submitted to the EMBL Data Library, July 1998
 A;Description: The sequence of C. elegans cosmid F12F3.
 A;Reference number: 221521
 A;Accession: T3416
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-2783 <FWL>
 A;Cross-references: EMBL:U80022; PIDN: AAC75886; 1; GSPDB: GN00023; CESP:F12F3.2
 A;Experimental source: Strain Bristol N2; clone F12F3
 C;Genetics:
 A;Gene: CESP:F12F3.2
 A;Map position: 5
 A;Introns: 45/3; 90/3; 451/3; 509/1; 2313/3; 2341/3; 2378/3; 2414/2; 2453/3; 2474/2; 252

RESULT 6
 T3416 hypothetical protein F12F3.2 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C;Accession: T3416
 R;Fulton, B.; Wohlgemann, P.
 Submitted to the EMBL Data Library, July 1998
 A;Description: The sequence of C. elegans cosmid F12F3.
 A;Reference number: 221521
 A;Accession: T3416
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-2783 <FWL>
 A;Cross-references: EMBL:U80022; PIDN: AAC75886; 1; GSPDB: GN00023; CESP:F12F3.2
 A;Experimental source: Strain Bristol N2; clone F12F3
 C;Genetics:
 A;Gene: CESP:F12F3.2
 A;Map position: 5
 A;Introns: 45/3; 90/3; 451/3; 509/1; 2313/3; 2341/3; 2378/3; 2414/2; 2453/3; 2474/2; 252

Query Match 35.1%; Score 605.5; DB 2; Length 371;
 Best Local Similarity 47.5%; Pred. No. 2.1e-20; Gaps 7;
 Matches 126; Conservative 61; Mismatches 69; Indels 9; Gaps 3;
 C;Species: Caenorhabditis elegans
 C;Accession: T3416
 R;Fulton, B.; Wohlgemann, P.
 Submitted to the EMBL Data Library, July 1998
 A;Description: The sequence of C. elegans cosmid F12F3.
 A;Reference number: 221521
 A;Accession: T3416
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-2783 <FWL>
 A;Cross-references: EMBL:U80022; PIDN: AAC75886; 1; GSPDB: GN00023; CESP:F12F3.2
 A;Experimental source: Strain Bristol N2; clone F12F3
 C;Genetics:
 A;Gene: CESP:F12F3.2
 A;Map position: 5
 A;Introns: 45/3; 90/3; 451/3; 509/1; 2313/3; 2341/3; 2378/3; 2414/2; 2453/3; 2474/2; 252

RESULT 7
 T3416 hypothetical protein F12F3.2 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Accession: T3416
 R;Fulton, B.; Wohlgemann, P.
 Submitted to the EMBL Data Library, July 1998
 A;Description: The sequence of C. elegans cosmid F12F3.
 A;Reference number: 221521
 A;Accession: T3416
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-2783 <FWL>
 A;Cross-references: EMBL:U80022; PIDN: AAC75886; 1; GSPDB: GN00023; CESP:F12F3.2
 A;Experimental source: Strain Bristol N2; clone F12F3
 C;Genetics:
 A;Gene: CESP:F12F3.2
 A;Map position: 5
 A;Introns: 45/3; 90/3; 451/3; 509/1; 2313/3; 2341/3; 2378/3; 2414/2; 2453/3; 2474/2; 252

Query Match 35.1%; Score 605.5; DB 2; Length 371;
 Best Local Similarity 47.5%; Pred. No. 2.1e-20; Gaps 7;
 Matches 126; Conservative 61; Mismatches 69; Indels 9; Gaps 3;
 C;Species: Caenorhabditis elegans
 C;Accession: T3416
 R;Fulton, B.; Wohlgemann, P.
 Submitted to the EMBL Data Library, July 1998
 A;Description: The sequence of C. elegans cosmid F12F3.
 A;Reference number: 221521
 A;Accession: T3416
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-2783 <FWL>
 A;Cross-references: EMBL:U80022; PIDN: AAC75886; 1; GSPDB: GN00023; CESP:F12F3.2
 A;Experimental source: Strain Bristol N2; clone F12F3
 C;Genetics:
 A;Gene: CESP:F12F3.2
 A;Map position: 5
 A;Introns: 45/3; 90/3; 451/3; 509/1; 2313/3; 2341/3; 2378/3; 2414/2; 2453/3; 2474/2; 252

RESULT 8
 T13931 projection - fruit fly (Drosophila melanogaster) (fragment)
 C;Species: drosophila melanogaster
 C;Accession: T13931
 R;Dalley, J.; Southgate, R.; Ayre-Southgate, A.
 J. Mol. Biol. 279, 201-210, 1998
 A;Title: Structure of the Drosophila protein: isoforms and implication for
 A;Reference number: 217815; MUID: 98300339
 A;Accession: T13931
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-6658 <DAL>
 A;Cross-references: EMBL:AF047475; PIDN: g3337430; PIDN: AAC27550.1
 C;Genetics:
 A;Gene: projectin
 A;Cross references: FlyBase: FBgn0005666
 A;Map position: 4
 A;Note: intron positions not resolved (incomplete sequence)
 C;Keywords: muscle

Query Match 35.2%; Score 650; DB 2; Length 6658;
 Best Local Similarity 42.9%; Pred. No. 2e-19; Gaps 5;
 Matches 139; Conservative 62; Mismatches 111; Indels 12; Gaps 5;

QY 6 QQQYEDFDPGEELGGSGFAIVKKCREKSTGGLEYAAKTFKKRROSRSRRGVSEEEFV 65
 |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 5707 QOSVYDRLDIEEGTGAFFGVHRCRERSTGNIFAKTIPVHS-----VERDLIREI 5760
 |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 QY 66 SILROYHLHWHWTHDVNTWDVWHLILWLGELFELP-FLAOKESSLBEATSFIQIL 124
 |||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 5761 DIMQQLHQLNLHDAFEDDEMILLEPLSGLGELFERITAEGYVMEAVINMRIC 5820
 |||:|||:|||:|||:|||:|||:
 QY 125 DGVNVYHHTKKTAHFEDIKPPENIMLDKNIPIPHILKIDSLAHELEDGEVFKNFGTPPRV 184
 |||:|||:|||:|||:|||:
 A;Residues: 1-371 <MAT>
 A;Accession: PC7178
 A;Molecule type: Protein
 A;Residues: 227-371 <MA2>
 A;Comment: This kinase, a novel calcineurin homologous protein (CHP) binding protein involved in the transfer of Na+/H+ exchanger 1 process and in some apoptotic events.
 C;Genetics:
 A;Gene: drck2
 C;Keywords: apoptosis

Db 5821 EGIRMHMEQNTITHDKTPENINCQTRS--STNVKLIDFGLATRLDPEVVKIT-TGIAEFG 5878
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 24-Sep-1999
 C;Accession: A35021; A05120; A25330
 R;Herring, B. P.; Stull, J.T.; Gallagher, P.J.
 J. Biol. Chem. 265, 1724-1730, 1990
 A;Title: Domain characterization of rabbit skeletal muscle myosin light chain kinase.
 A;Reference number: A35021; MUID:90110242
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-608 <HER>
 A;Cross-references: GB:J05194; NID:9165505; PID:AAA1400_1; PID:9165505
 R;Takio, K.; Blumenthal, D.K.; Edelman, A.M.; Walsh, K.A.; Krebs, E.G.; Titani, K.
 Biochemistry 24, 6028-6037, 1985
 A;Title: Amino acid sequence of rabbit skeletal muscle myosin light chain kinase.
 A;Reference number: A05120; MUID:86104095
 A;Accession: A05120
 A;Molecule type: protein
 A;Residues: 237-604 <TRK>
 R;Takio, K.; Blumenthal, D.K.; Walsh, K.A.; Titani, K.; Krebs, E.G.
 Biochemistry 25, 8049-8057, 1986
 A;Title: Amino acid sequence of rabbit skeletal muscle myosin light chain kinase.
 A;Reference number: A25830; MUID:87101105
 A;Accession: A25830
 A;Molecule type: protein
 A;Residues: 2-336, 'K', 337-604 <TA2>
 C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; Protein kinase homolog
 C;Keywords: ATP; muscle; phosphotransferase; serine/threonine-specific protein kinase
 F:295-552/Domain: protein kinase homology <KIN>
 F:303-311/Region: protein kinase ATP-binding motif

Query Match 33.7%; Score 621.5; DB 2; Length 451;
 Best Local Similarity 46.0%; Pred. No. 2.6e-19;
 Matches 125; Conservative 50; Mismatches 88; Indels 9; Gaps 3;

Db 39 KQGSCPDYDIEELGGAFGVYHRCEVAKGRFEKFIN----TPYPLDKYVNE 92
 Qy 65 VSILRQLVHHNNTLHDVYVENTDVWHLLELVSGGELDFELAQKE-SLSBEEATSFIKQIOLDGVNLHTRKI 123
 93 ISIMNQLHHPKLINLDAFEDKDMVILEFLPSGGELFDRIAAEDYKMSEREVINMRQA 152

Db 153 CEGLKHHHEHSVHLDIKPENIMCETRK--ASSVKIDGLATKLNDETVTTAEP 210
 Qy 184 VAPENVYEPGLEADMSIGVITYILSGASPFGLDTKOETLANTITSVSDPDEEFFSH 243
 Db 211 AAPEIVDREPVGFYTDWAIGVLYLLSGSLSPAGEEDDTLQNYKRCDDWFEDAFSS 270
 Qy 244 TSELAKDFIRKLVKRKRTRIQEALRHPWT 275
 Db 271 VSPPEAKDFIKNLQKPRKRITVHDALEHPU 302

RESULT 10
 A35021 myosin-light-chain kinase (EC 2.7.1.117), skeletal muscle - rabbit

Db 5999 FERFLIPIGRULSEYSSLRKLMER 6022

RESULT 9
 S49128 twitchin-like protein - California sea hare (fragment)
 C;Species: Aplysia californica (California sea hare)
 C;Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 17-Nov-2000
 C;Accession: S49128; A53923
 R;Heierhorst, J.; Probst, W.C.; Wilim, F.S.; Buku, A.; Weiss, K.R.
 submitted to the EMBL Data Library, February 1994
 A;Description: Autophosphorylation of molluscan twitchin and interaction of its kinase domain
 A;Reference number: A53923
 A;Accession: S49128
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-451 <HER>
 A;Cross-references: ENBL:230161; NID:9509412; PID:CAA82911_1; PID:9509413
 R;Heierhorst, J.; Probst, W.C.; Wilim, F.S.; Buku, A.; Weiss, K.R.
 J. Biol. Chem. 269, 21086-21093, 1994
 A;Title: Autophosphorylation of molluscan twitchin and interaction of its kinase domain
 A;Reference number: A53923; MUID:94342273
 A;Accession: A53923
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 5-372 <HER>
 A;Cross-references: GB:J230161
 C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; Protein kinase homolog
 C;Keywords: ATP; muscle; phosphotransferase; serine/threonine-specific protein kinase
 F:53-61/Region: protein kinase ATP-binding motif

Query Match 32.8%; Score 605; DB 2; Length 608;
 Best Local Similarity 40.4%; Pred. No. 1.6e-18;
 Matches 124; Conservative 63; Mismatches 106; Indels 14; Gaps 5;

Db 301 EAAGGGKGAVCHTCSTEKTGKLAKVKKOPK-----DKEMVMLIEVNOMLNHRL 354
 Qy 77 ITLHDVYENRTDVWHLLELVSGGELDFELAQKE-SLSBEEATSFIKQIOLDGVNLHTRKI 135
 Db 355 IQYAAETPHEVLFMVEYIEGGELFERIVDYEYLVEVDTMVFVRICIDGLFMHMRRV 414
 Qy 136 AHEDLKPENIMLKDNTIPIHTKLIDRGLAHEIEDGYEFKNFTGTPERVAPEIINYPLG 195
 Db 415 LHDLKPKENILCVNTTGHL--VKIDFLGFLARRYNPNEKLVNGFTPERLSPEVNYDOIS 472
 Qy 196 LEADMWSGVITYILSGASPFGLDTKOETLANTITSVSDPDEEFFSHTESELAKEFIRKL 255
 Db 473 DKTDMSLGSVITYMLSGSLSPGDDDTETLNNVLWSGNWYFBETTERAVSDEAKDFVNSL 532
 Qy 256 LVKETRKRLTQEALRHPWTIPVDNQQAMRR--ESVVMLENERKQVRRRKLKSFSIVS 313
 Db 533 IVEQGAMSAQCLAHFWLNNAEAKRCNRRLKSQLILL--KRYLMKRRKKNFAVS 589
 Qy 314 LCNHLTR 320
 Db 590 AANRFKK 596

RESULT 11
 A28798 myosin-light-chain kinase (EC 2.7.1.117), skeletal muscle - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Accession: A28798; A60441
 R;Roush, C.L.; Kennedy, P.J.; Giaccum, M.B.; Helfman, D.M.; Scott, J.D.; Krebs, E.G.
 J. Biol. Chem. 263, 10510-10516, 1988
 A;Title: Isolation of the cDNA encoding rat skeletal muscle myosin light chain kinase
 A;Reference number: A28798
 A;Accession: A28798; MUID:88273159
 A;Molecule type: mRNA

Query Match 32.7%; Score 604; DB 2; Length 610;
Best Local Similarity 39.1%; Pred. No. 1.8e-18; Matches 120; Conservative 67; Mismatches 106; Indels 14; Gaps 5;

Db 303 EALGGKFGAVCTCITERSTGKLAKVVIKKQTP-----DKENVILLEFVMNOLNHLN 356

Qy 17 EBLGSQFAITVKCREFKSTGLEYAAFKIKRQSRASRGSREELEREVSIILRQLVHLHN 75

Db 357 IQLYSATETSHIELMFMEYIEGGELFERIVDQEYOLTEVDTMFWRQICGILFNHHKMRV 416

Qy 136 AIFDLKENTIMLDKNIPPIPHKLIDGLAHETDGVEFKNFGTPEVAPEIVNVEPLG 195

Db 417 LHDLKPNENLIVQVTHGL--VKKIDEGLARRKYNPKNEKLKINGFPEFLSPVVVWQIS 474

Qy 196 LEADMWSIGVITYILSGASPRPLGDPKQETANLTTSVSYDFDEEFSHTSBLAKDPIKL 255

Db 475 DKTDMWSLGIVTYMLLSGLSPFLGDDDTETLNINVNLANSWIFDEEFFAEVSDAKDEVSNL 534

Qy 256 LVKETRKRLTQEARLHPWITVNDQAMVR--ESVNLENFRKGYVURRKWLFSIVS 313

Db 535 ITKQDQSARMSAECOCLAHPLWNLNLAEKAKRCNRKLKSQILL---KKYLMKRWKRNKFIAVS 591

Qy 314 LCNHLTR 320

Db 592 ANRFFK 598

RESULT 12

T27522 hypothetical protein zc273.4 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T27522
R;Kershaw, J.
submitted to the EMBL data library April 1995
A;Reference number: Z20382
A;Accession: T27522
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1211 <WIL>
A;Cross-references: EMBL:Z249131; PIDN:CAA88976.1; GSPDB:GN00028; CESP:ZC373.4
A;Experimental source: clone ZC373
C;Genetics: CESP:ZC373.4
A;Gene: CESP:ZC373.4
A;Map Position: X
A;Introns: 20/1; 53/2; 80/3; 122/2; 169/3; 236/2; 286/2; 337/3; 381/3; 402/3; 445

Query Match 31.7%; Score 584.5; DB 2; Length 631;
Best Local Similarity 42.0%; Pred. No. 1e-16; Matches 115; Conservative 52; Mismatches 98; Indels 9; Gaps 3;

Db 5926 KHDVHVDYTHEELGIGAFGVWHRTERATGNNPAFKVWMPHES-----DKETVRIKE 5979

Qy 65 VSLRQLHHNVITLHDVYERNTDVHILEVSGGLEFLDFLAKES-LSEBEATSFIKOI 123

Db 5980 IOTMSVLHPTVLNLDHADFEODINEMVYIYFMSGGELFERKVADEINKMSDEAVYMRQV 6039

Qy 124 LDGVNLYLHKKTAHFDLKENTIMLDKNIPPIPHKLIDGLAHETDGVEFKNFGTPEV 183

Db 6040 CKGLCHMHMHENYVHDLKPNENIMFTKR--SNEKLIDFLGTAAHLDPKOSVKTGTAEF 6097

Qy 184 VAREIVNVEPLGLEDAMWSIGVITYILSGASPRPLGDTQETANLTTSVSYDFDEEFFSH 243

Db 6098 AAPEVAECKPVGYTDWMSGVSYILSGLSPFGGENDDETLLRNVKSCDNWMDSAFG 6157

Qy 244 TSBLAKDTRKLKVETRKRLTQEARLHPWITP 277

Db 6158 ISEDGKDFIRKLJLADPRTMTHQALHPWITP 6191

Query Match 31.9%; Score 589; DB 2; Length 1211;
Best Local Similarity 41.2%; Pred. No. 1.e-17; Matches 140; Conservative 48; Mismatches 112; Indels 40; Gaps 8;

Db 8 KVEDFDIGEGLSGOFATVKCREFKSTGLEYAAFKIKRQSRASRGSREELEREVSI 67

Db 40 KFDTLQVTKLIGDSFGKVVCVIRETGKFAFK-----IRKAEADREVERVSI 93

RESULT 14

S5742 twitchin [similarity] - *Caenorhabditis elegans*

N Alternate name: myosin regulating protein
 N Contains: protein kinase (EC 2.7.1.-)
 C Species: *Caenorhabditis elegans*
 C Date: 28-Oct-1995 #sequence_revision 24-Oct-1997 #text_change 20-Jun-2000
 C Accession: S57242; T07571; S07979; S57218; T27934; T28030
 R Benian, G.M.; L'Herault, S.W.; Morris, M.E.
 submitted to the EMBL Data Library, February 1993
 A Description: Additional sequence complexity within twitching of *Caenorhabditis elegans*
 A Accession: S57242
 A Molecule type: DNA
 A Residues: 1-6839 <BEN1>
 A Cross-references: EMBL:L10351
 A Experimental source: var. Bristol
 R Benian, G.
 submitted to the EMBL Data Library, November 1989
 A Reference number: SU07571
 A Accession: S07571
 A Molecule type: DNA
 A Residues: 792-6839 <BEN2>
 A Cross-references: EMBL:X15423; NID:96897; PIDN:CAA33463.1; PID:96898
 A Experimental source: var. Bristol
 R Benian, G.M.; Kiff, J.E.; Neckelmann, N.; Moerman, D.G.; Waterston, R.H.
 Nature 342, 45-50, 1999
 A Title: Sequence of an unusually large protein implicated in regulation of myosin activ
 A Reference number: SU06797; MUIB:90044042
 A Status: nucleic acid sequence not shown
 A Accession: S06797
 A Molecule type: DNA
 A Residues: 806-1175; 1178-1998, 'Y', 2000-3040, 'I', 3042-3335, 'I', 3337-5693; 5696-6359, 'I', 6
 A Cross-references: EMBL:X15423
 A Experimental source: var. Bristol
 R Benian, G.M.; L'Herault, S.W.; Morris, M.E.
 Genetics 134: 1097-1104, 1993
 A Title: Additional sequence complexity in the muscle gene, unc-22, and its encoded prot
 A Reference number: S57218; MUIB:93397664
 A Accession: S57218
 A Molecule type: DNA
 A Residues: 2-99-108-194, 'Q', 196-206; 374-468; 658-753 <BEN4>
 A Status: preliminary; translated from GB/EMBL/DDBJ
 R White, S.
 Submitted to the EMBL Data Library, May 1996
 A Reference number: Z20442
 A Accession: T27934
 A Status: preliminary; translated from GB/EMBL/DDBJ
 A Molecule type: DNA
 A Residues: 'MGIROKCKQ', 19-6839 <WIL>
 A Cross-references: EMBL:Z73897; PIDN:CAA98064.1; GSPDB:GN00022; CESP:ZK617.1a
 A Experimental source: clone ZK617
 R Harris, B.
 submitted to the EMBL Data Library, May 1996
 A Reference number: Z20458
 A Accession: T28030
 A Status: preliminary; translated from GB/EMBL/DDBJ
 A Molecule type: DNA
 A Residues: 'MGIROKCKQ', 19-6839 <WIL>
 A Cross-references: EMBL:Z73899; PIDN:CAA98081.1; GSPDB:GN00022; CESP:ZK617.1a
 A Experimental source: clone ZK617
 C Comment: Lack of unc-22 leads to a constant twitching of the body muscles.
 C Genetics:
 A Gene: unc-22; CESP:ZK617.1a
 A Map position: 4
 A Introns: 18/3; 69/3; 143/2; 176/3; 264/2; 387/3; 413/2; 471/1; 516/3; 550/3; 582/3; 60
 C Superfamily: twitchin; fibronectin type III repeat homology; immunoglobulin homology;
 C Keywords: ATP; autophosphorylation; duplication; muscle; phosphotransferase; sexine/tt
 F 806-898-899-990-991-1083-1084-1175-1178-1273-1474-1567-1770-1864-2066-2158-2358-2450-2
 F 6265-6265-6356-6385-6478-6541-6635-6649-6742-6745-6839; Region: motif 2
 F 1274-1372-1373-1473-1568-1670-1671-1769-1865-1964-1965-2065-2159-2258-2259-2357-2451-2
 F 3-4215-4313-4314-4415-4416-4516-4612-4710-4711-4811, 4908-5009, 5010-5109, 5110-5210, 5399-
 F 5940-6167-
 F 5948-5956-Region: protein kinase homology <KIN>
 F 5971/Active site: Lys #status predicted

Query	Match	31.7%	Score	584.5;	DB	2;	Length	6839;
	Best Local Similarity	42.0%	Pred	NO.	1..1e-16;			
	Matches	115;	Conservative	52;	Mismatches	98;	Indels	9;
							Gaps	3;
QY	5	KQQKVEDPYDIEGLSGQFATVKKCRKSTGLEYAAFKIKKQRSARRGVSRREERE	64					
Db	5934	KHDHVLDHYDHIBLGAGFVGVRVTRATGNNFAAKFMPHES	--D-KETWKE	5987				
QY	65	VSTLQRQVHNNTLHDYENRTDVHLLPELGAKES-LSEEEATSFROI	123					
Db	5988	IOTMSVLRLHPTLVNLHDAPEDDNEMVMYEFMGGELEFKADEHNKNNSDEAVEYMRQV	6047					
QY	124	LDGVNYLTTKKAHFPLPENIMLDKIPKIPKLDFGLAHIEOGEVFRNIFCPPE	183					
Db	6048	CKGLCHMMHENNVYHDLKIPNEMTTR--SNEKLIDFLGTLAHDLPQSVKVTGTAEP	6105					
QY	184	VAPBIVNVEPLGLQADMMASIGVITYILSGASPLGLDTKQETANISVSYDEDEEFSH	243					
Db	6106	AAPEVAEKGPKPGVYTDMMSVGSVLSLGLSPFGGENDETURNVKSCDWMDSDAERG	6165					
QY	244	TSELAKDFTTKLAKVETKRTQALRHPWITP	277					
Db	6166	ISEDGKDFTKLLADPWTMTHQALEHHPWLTP	6199					
RESULT	15							
T27935		hypothetical protein ZK617.1b - <i>Caenorhabditis elegans</i>						
C;Species:		<i>Caenorhabditis elegans</i>						
C;Date:		15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000						
C;Accession:		T27935; T28031						
R;White, S.								
A;Reference number:		submitted to the EMBL Data Library, May 1996						
A;Accession:		Z20442						
A;Status:		preliminary; translated from GB/EMBL/DDBJ						
A;Molecule type:		DNA						
A;Residues:		1-1760 <WIL>						
A;Cross-references:		EMBL:Z73897; PIDN:CAA98065.1; GSPDB:GN00022; CESP:ZK617.1b						
A;Experimental source:		clone ZK617						
R;Harris, B.								
A;Submitted to the EMBL Data Library, May 1996								
A;Reference number:		Z20458						
A;Accession:		T28031						
A;Status:		preliminary; translated from GB/EMBL/DDBJ						
A;Molecule type:		DNA						
A;Residues:		1-1760 <WIL>						
A;Cross-references:		EMBL:Z73899; PIDN:CAA98082.1; GSPDB:GN00022; CESP:ZK617.1b						
A;Experimental source:		clone ZK829						
C;Genetics:								
A;Gene:		CESP:ZK617.1b						
A;Map position:		4						
A;Introns:		18/3; 69/3; 143/2; 176/3; 264/2; 387/3; 413/2; 471/1; 516/3; 550/3; 582/3; 60						
C;Superfamily:		twitchin; fibronectin type III repeat homology; immunoglobulin homology;						
C;Keywords:		ATP; autophosphorylation; duplication; muscle; phosphotransferase; sexine/tt						
F 806-898-899-990-991-1083-1084-1175-1178-1273-1474-1567-1770-1864-2066-2158-2358-2450-2								
F 6265-6265-6356-6385-6478-6541-6635-6649-6742-6745-6839; Region: motif 2								
F 1274-1372-1373-1473-1568-1670-1671-1769-1865-1964-1965-2065-2159-2258-2259-2357-2451-2								
F 3-4215-4313-4314-4415-4416-4516-4612-4710-4711-4811, 4908-5009, 5010-5109, 5110-5210, 5399-								
F 5940-6167- F 5948-5956-Region: protein kinase homology <KIN>								
F 5971/Active site: Lys #status predicted								
QY	124	LDGVNYLTTKKAHFPLPENIMLDKIPKIPKLDFGLAHIEOGEVFRNIFCPPE	183					

Sat May 18 15:09:08 2002

11S-09-719-748-2.FBR

Db	6369	CKGLCHMHENNYVHDLKPKENIMETTKR--SNEKLKDGFGLAHDLPDKQSIVKWTGTAEF	6426
Qy	184	VAPETVNYPLGLPBMADMSIGVITYIILSGASPLGDTKQETLANTISVSYDDERFSH	243
		: : : : : : : : :	
Db	6427	AAPEVAEGKPGVYTDMMWSVGVISYIILSGLSPFGGENDETURNVSCDWNMDSAFSG	6486
Qy	244	TSELAKDFRKLUVKLUKETRKRLTOEARHPWITP	277
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Db	6487	ISEDGKDETRKLЛАDPNTRMTIQALEHFWLTP	6520

Search completed: May 18, 2002, 04:49:59
Job time: 9105 sec